

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel Screening Method

<130> P04-117PCT

<150> JP 2002-093045

<151> 2002-03-28

<150> JP 2002-361580

<151> 2002-12-13

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 957

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1)..(957)

<223> rat-derived rCB7T084

<400> 1

atg aac tac act cct tat agc agc cca gcc cca ggt ctg acc atc agc	48
Met Asn Tyr Thr Pro Tyr Ser Ser Pro Ala Pro Gly Leu Thr Ile Ser	
1 5 10 15	
ccc acc atg gac cct gtg acc tgg gtt tac ttt tca gtg aca ttc ctg	96
Pro Thr Met Asp Pro Val Thr Trp Val Tyr Phe Ser Val Thr Phe Leu	
20 25 30	
gcc atg gcc acc tgt gtg tgt ggg ata gtg ggc aac tcc atg gtg att	144
Ala Met Ala Thr Cys Val Cys Gly Ile Val Gly Asn Ser Met Val Ile	

35	40	45	
tgg cta ctg agt ttc cac agt	gtg cag agg tcc ccc ttc tgc acc tac	192	
Trp Leu Leu Ser Phe His Ser Val Gln Arg Ser Pro Phe Cys Thr Tyr			
50	55	60	
gtg ctc aac ctg gcg gtg gcc gac ctc ctc ttc ctg ctc tgc atg gcc	240		
Val Leu Asn Leu Ala Val Ala Asp Leu Leu Phe Leu Leu Cys Met Ala			
65	70	75	80
tcc ctg ctc agt ctg gaa aca ggg ccc ctg ctc aca gcc agc acc tcc	288		
Ser Leu Leu Ser Leu Glu Thr Gly Pro Leu Leu Thr Ala Ser Thr Ser			
85	90	95	
gcc aga gtc tac gag ggg atg aag aga atc aag tac ttt gcc tac aca	336		
Ala Arg Val Tyr Glu Gly Met Lys Arg Ile Lys Tyr Phe Ala Tyr Thr			
100	105	110	
gca ggc ctg agc ctg ctg acg gcc atc agc acc cag cgc tgt ctc tcc	384		
Ala Gly Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser			
115	120	125	
gtg ctt ttc ccc atc tgg tat aag tgc cac cgg ccc cag cac ctg tcg	432		
Val Leu Phe Pro Ile Trp Tyr Lys Cys His Arg Pro Gln His Leu Ser			
130	135	140	
ggg gtg gta tgt ggt gtg ctg tgg gca ctg gcc ctc ctg atg aac ttc	480		
Gly Val Val Cys Gly Val Leu Trp Ala Leu Ala Leu Leu Met Asn Phe			
145	150	155	160
ctg gct tct ttc ttc tgt gtt caa ttc tgg cat ccc gac aaa tac cag	528		
Leu Ala Ser Phe Phe Cys Val Gln Phe Trp His Pro Asp Lys Tyr Gln			
165	170	175	
tgc ttc aag gtg gac atg gtt ttc aac agt ctt atc ctg ggg atc ttc	576		
Cys Phe Lys Val Asp Met Val Phe Asn Ser Leu Ile Leu Gly Ile Phe			
180	185	190	
atg ccc gtc atg gtc ctg acc agc gcc atc atc ttc atc cgc atg cga	624		
Met Pro Val Met Val Leu Thr Ser Ala Ile Ile Phe Ile Arg Met Arg			
195	200	205	
aag aac agc ctg ctg cag aga cgg cag cct cgg cgg ctc tac gtg gtc	672		
Lys Asn Ser Leu Leu Gln Arg Arg Gln Pro Arg Arg Leu Tyr Val Val			
210	215	220	
atc ctg act tcc gtc ctt gtc ttc ctt acc tgt tct ctg ccg ttg ggc	720		
Ile Leu Thr Ser Val Leu Val Phe Leu Thr Cys Ser Leu Pro Leu Gly			
225	230	235	240

atc aac tgg ttc tta ctc tac tgg gtg gaa ctg ccg cag gcc gtg agg 768
 Ile Asn Trp Phe Leu Leu Tyr Trp Val Glu Leu Pro Gln Ala Val Arg
 245 250 255
 ctc ctg tac gtc tgc tca tca cgc ttc tcc tcg tct ttg agc agc agc 816
 Leu Leu Tyr Val Cys Ser Ser Arg Phe Ser Ser Ser Leu Ser Ser Ser
 260 265 270
 gcc aac cca gtc atc tac ttc ctc gtg ggc agc cag aag agc cac cgg 864
 Ala Asn Pro Val Ile Tyr Phe Leu Val Gly Ser Gln Lys Ser His Arg
 275 280 285
 ctg cag gag tct ctg ggt gct gtg ctg ggg cgg gca ctt cag gac gag 912
 Leu Gln Glu Ser Leu Gly Ala Val Leu Gly Arg Ala Leu Gln Asp Glu
 290 295 300
 cct gaa ggc agg gag acg cca tcc aca tgt act aat gat ggg gtc 957
 Pro Glu Gly Arg Glu Thr Pro Ser Thr Cys Thr Asn Asp Gly Val
 305 310 315

<210> 2

<211> 319

<212> PRT

<213> Rattus sp.

<400> 2

Met Asn Tyr Thr Pro Tyr Ser Ser Pro Ala Pro Gly Leu Thr Ile Ser
 1 5 10 15
 Pro Thr Met Asp Pro Val Thr Trp Val Tyr Phe Ser Val Thr Phe Leu
 20 25 30
 Ala Met Ala Thr Cys Val Cys Gly Ile Val Gly Asn Ser Met Val Ile
 35 40 45
 Trp Leu Leu Ser Phe His Ser Val Gln Arg Ser Pro Phe Cys Thr Tyr
 50 55 60
 Val Leu Asn Leu Ala Val Ala Asp Leu Leu Phe Leu Leu Cys Met Ala
 65 70 75 80
 Ser Leu Leu Ser Leu Glu Thr Gly Pro Leu Leu Thr Ala Ser Thr Ser
 85 90 95
 Ala Arg Val Tyr Glu Gly Met Lys Arg Ile Lys Tyr Phe Ala Tyr Thr
 100 105 110
 Ala Gly Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser

115	120	125
Val Leu Phe Pro Ile Trp Tyr Lys Cys His Arg Pro Gln His Leu Ser		
130	135	140
Gly Val Val Cys Gly Val Leu Trp Ala Leu Ala Leu Leu Met Asn Phe		
145	150	155
Leu Ala Ser Phe Phe Cys Val Gln Phe Trp His Pro Asp Lys Tyr Gln		
165	170	175
Cys Phe Lys Val Asp Met Val Phe Asn Ser Leu Ile Leu Gly Ile Phe		
180	185	190
Met Pro Val Met Val Leu Thr Ser Ala Ile Ile Phe Ile Arg Met Arg		
195	200	205
Lys Asn Ser Leu Leu Gln Arg Arg Gln Pro Arg Arg Leu Tyr Val Val		
210	215	220
Ile Leu Thr Ser Val Leu Val Phe Leu Thr Cys Ser Leu Pro Leu Gly		
225	230	235
Ile Asn Trp Phe Leu Leu Tyr Trp Val Glu Leu Pro Gln Ala Val Arg		
245	250	255
Leu Leu Tyr Val Cys Ser Ser Arg Phe Ser Ser Ser Leu Ser Ser Ser		
260	265	270
Ala Asn Pro Val Ile Tyr Phe Leu Val Gly Ser Gln Lys Ser His Arg		
275	280	285
Leu Gln Glu Ser Leu Gly Ala Val Leu Gly Arg Ala Leu Gln Asp Glu		
290	295	300
Pro Glu Gly Arg Glu Thr Pro Ser Thr Cys Thr Asn Asp Gly Val		
305	310	315

<210> 3

<211> 963

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(963)

<223> human-derived TGR7

<400> 3

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Met Asn Gln Thr Leu Asn Ser Ser Gly Thr Val Glu Ser Ala Leu Asn	
1 5 10 15	
tat tcc aga ggg agc aca gtg cac acg gcc tac ctg gtg ctg agc tcc	96
Tyr Ser Arg Gly Ser Thr Val His Thr Ala Tyr Leu Val Leu Ser Ser	
20 25 30	
ctg gcc atg ttc acc tgc ctg tgc ggg atg gca ggc aac agc atg gtg	144
Leu Ala Met Phe Thr Cys Leu Cys Gly Met Ala Gly Asn Ser Met Val	
35 40 45	
atc tgg ctg ctg ggc ttt cga atg cac agg aac ccc ttc tgc atc tat	192
Ile Trp Leu Leu Gly Phe Arg Met His Arg Asn Pro Phe Cys Ile Tyr	
50 55 60	
atc ctc aac ctg gcg gca gcc gac ctc ctc ttc ctc ttc agc atg gct	240
Ile Leu Asn Leu Ala Ala Ala Asp Leu Leu Phe Leu Phe Ser Met Ala	
65 70 75 80	
tcc acg ctc agc ctg gaa acc cag ccc ctg gtc aat acc act gac aag	288
Ser Thr Leu Ser Leu Glu Thr Gln Pro Leu Val Asn Thr Thr Asp Lys	
85 90 95	
gtc cac gag ctg atg aag aga ctg atg tac ttt gcc tac aca gtg ggc	336
Val His Glu Leu Met Lys Arg Leu Met Tyr Phe Ala Tyr Thr Val Gly	
100 105 110	
ctg agc ctg ctg acg gcc atc agc acc cag cgc tgt ctc tct gtc ctc	384
Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser Val Leu	
115 120 125	
ttc cct atc tgg ttc aag tgt cac cgg ccc agg cac ctg tca gcc tgg	432
Phe Pro Ile Trp Phe Lys Cys His Arg Pro Arg His Leu Ser Ala Trp	
130 135 140	
gtg tgt ggc ctg ctg tgg acg ctc tgt ctc ctg atg aac ggg ttg acc	480
Val Cys Gly Leu Leu Trp Thr Leu Cys Leu Leu Met Asn Gly Leu Thr	
145 150 155 160	
tct tcc ttc tgc agc aag ttc ttg aaa ttc aat gaa gat cgg tgc ttc	528
Ser Ser Phe Cys Ser Lys Phe Leu Lys Phe Asn Glu Asp Arg Cys Phe	
165 170 175	
agg gtg gac atg gtc cag gcc gcc ctc atc atg ggg gtc tta acc cca	576
Arg Val Asp Met Val Gln Ala Ala Leu Ile Met Gly Val Leu Thr Pro	
180 185 190	
gtg atg act ctg tcc agc ctg acc ctc ttt gtc tgg gtg cgg agg agc	624

Val Met Thr Leu Ser Ser Leu Thr Leu Phe Val Trp Val Arg Arg Ser	
195 200 205	
tcc cag cag tgg cgg cgg cag ccc aca cgg ctg ttc gtg gtg gtc ctg	672
Ser Gln Gln Trp Arg Arg Gln Pro Thr Arg Leu Phe Val Val Val Leu	
210 215 220	
gcc tct gtc ctg gtg ttc ctc atc tgt tcc ctg cct ctg agc atc tac	720
Ala Ser Val Leu Val Phe Leu Ile Cys Ser Leu Pro Leu Ser Ile Tyr	
225 230 235 240	
tgg ttt gtg ctc tac tgg ttg agc ctg ccg ccc gag atg cag gtc ctg	768
Trp Phe Val Leu Tyr Trp Leu Ser Leu Pro Pro Glu Met Gln Val Leu	
245 250 255	
tgc ttc agc ttg tca cgc ctc tcc tcg tcc gta agc agc agc gcc aac	816
Cys Phe Ser Leu Ser Arg Leu Ser Ser Ser Val Ser Ser Ser Ala Asn	
260 265 270	
ccc gtc atc tac ttc ctg gtg ggc agc cgg agg agc cac agg ctg ccc	864
Pro Val Ile Tyr Phe Leu Val Gly Ser Arg Arg Ser His Arg Leu Pro	
275 280 285	
acc agg tcc ctg ggg act gtg ctc caa cag gcg ctt cgc gag gag ccc	912
Thr Arg Ser Leu Gly Thr Val Leu Gln Gln Ala Leu Arg Glu Glu Pro	
290 295 300	
gag ctg gaa ggt ggg gag acg ccc acc gtg ggc acc aat gag atg ggg	960
Glu Leu Glu Gly Gly Glu Thr Pro Thr Val Gly Thr Asn Glu Met Gly	
305 310 315 320	
gct	963
Ala	

<210> 4

<211> 321

<212> PRT

<213> Homo sapiens

<400> 4

Met Asn Gln Thr Leu Asn Ser Ser Gly Thr Val Glu Ser Ala Leu Asn	
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Tyr Ser Arg Gly Ser Thr Val His Thr Ala Tyr Leu Val Leu Ser Ser	
20 25 30	
Leu Ala Met Phe Thr Cys Leu Cys Gly Met Ala Gly Asn Ser Met Val	

35	40	45
Ile Trp Leu Leu Gly Phe Arg Met His Arg Asn Pro Phe Cys Ile Tyr		
50	55	60
Ile Leu Asn Leu Ala Ala Ala Asp Leu Leu Phe Leu Phe Ser Met Ala		
65	70	75
Ser Thr Leu Ser Leu Glu Thr Gln Pro Leu Val Asn Thr Thr Asp Lys		
85	90	95
Val His Glu Leu Met Lys Arg Leu Met Tyr Phe Ala Tyr Thr Val Gly		
100	105	110
Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser Val Leu		
115	120	125
Phe Pro Ile Trp Phe Lys Cys His Arg Pro Arg His Leu Ser Ala Trp		
130	135	140
Val Cys Gly Leu Leu Trp Thr Leu Cys Leu Leu Met Asn Gly Leu Thr		
145	150	155
Ser Ser Phe Cys Ser Lys Phe Leu Lys Phe Asn Glu Asp Arg Cys Phe		
165	170	175
Arg Val Asp Met Val Gln Ala Ala Leu Ile Met Gly Val Leu Thr Pro		
180	185	190
Val Met Thr Leu Ser Ser Leu Thr Leu Phe Val Trp Val Arg Arg Ser		
195	200	205
Ser Gln Gln Trp Arg Arg Gln Pro Thr Arg Leu Phe Val Val Val Leu		
210	215	220
Ala Ser Val Leu Val Phe Leu Ile Cys Ser Leu Pro Leu Ser Ile Tyr		
225	230	235
Trp Phe Val Leu Tyr Trp Leu Ser Leu Pro Pro Glu Met Gln Val Leu		
245	250	255
Cys Phe Ser Leu Ser Arg Leu Ser Ser Ser Val Ser Ser Ser Ala Asn		
260	265	270
Pro Val Ile Tyr Phe Leu Val Gly Ser Arg Arg Ser His Arg Leu Pro		
275	280	285
Thr Arg Ser Leu Gly Thr Val Leu Gln Gln Ala Leu Arg Glu Glu Pro		
290	295	300
Glu Leu Glu Gly Gly Glu Thr Pro Thr Val Gly Thr Asn Glu Met Gly		
305	310	315
Ala		320

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 5

ggctttcgaa tgcacaggaa

20

<210> 6

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Primer

<400> 6

cgtggaagcc atgctgaag

19

<210> 7

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe, labeled 5'-terminal with FAM and 3'-terminal with TAMRA

<400> 7

ttctgcatct atatcctcaa cctggcgg

28

<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 8

tgatgaactt cctggcttct ttc 23

<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 9

tgtccacctt gaagcactgg ta 22

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Probe, labeled 5'-terminal with FAM and 3'-terminal with TAMRA

<400> 10

ctgtgttcaa ttctggcatc ccgacaa 27